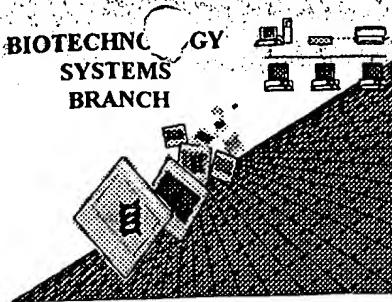


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/770,517

Source: OIPE

Date Processed by STIC: 7/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/770,517</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

Field 220 must be blank.

Field 221 must include a term from the name/key table 5 or 6

Field 222 must specify a location in the nucleic acid sequence

Field 223 must include ~~values of~~ description of a and any other description in your own words up to 4 lines of text.

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001
TIME: 13:48:46

Input Set : A:\06501-072001.txt
Output Set: N:\CRF3\07252001\I770517.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Mitsuhashi, Kazuya
5 Yamamoto, Hiroaki
6 Matsuyama, Akinobu
7 Tokuyama, Shinji
9 <120> TITLE OF INVENTION: D-AMINOACYLASE AND GENE ENCODING THE SAME
11 <130> FILE REFERENCE: 06501-072001
13 <140> CURRENT APPLICATION NUMBER: US 09/770,517
14 <141> CURRENT FILING DATE: 2001-01-26
16 <150> PRIOR APPLICATION NUMBER: JP 2000-019080
17 <151> PRIOR FILING DATE: 2000-01-27
19 <150> PRIOR APPLICATION NUMBER: JP 2000-150578
20 <151> PRIOR FILING DATE: 2000-05-22
22 <160> NUMBER OF SEQ ID NOS: 27
24 <170> SOFTWARE: PatentIn Ver. 2.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1677
28 <212> TYPE: DNA
29 <213> ORGANISM: Hypomyces mycophilus
31 <400> SEQUENCE: 1
32 atgcggactg aaattcttcc caactcagcc actgttatca cggcgatga agcagccag 60
33 ccctttgtgg ccgatgtgct ggttcgaag ggactgattg ccaagattgg taaccccggt 120
34 tccatcaatg caactccaga tacgcggcat ctcgacgtca caggctacat tctatetcct 180
35 gtttcatcg atatgcatgc gcattcagac ctctacctac tctctcatcc tgaccacgag 240
36 gccaaaatca cccaaggatg cacaacggaa gttgtggcc aagacggat atcatatgca 300
37 ccaattcgtat atgttagacca gttgagggcg atccgagaac agattgctgg atggaatggc 360
38 aatcctacag atgaggagtg cggacaact ctcaaaaggcg ttggcatgtt tgaatggcag 420
39 actattgggg aataacttggta ttgtttggag agaaacagga cggccactaa tgcgcgcatt 480
40 ttggttccgc aaggcaacct gagattattt gcatgtggcc catacgatac tccagcatct 540
41 gcagaagaga ttcaagatca aatccagctc ttgcgagagg ctatggctca ggtgtctgtc 600
42 gggatgtcta gtggctcac ttatacaccc ggcatgtatg cttccacgtc ggaactagct 660
43 tctctgtcgcc cgccctcgca acaagaattt ccaggtgcatt tctatgcgcc acatcataga 720
44 agttatgggt tccaggccat cgaaagttat gccaaatgt tggatctcg agagtcaaca 780
45 ggctgtccca ttcatcttac acatgcaacg ctcaactttt cagaaaataaa ggttaaagct 840
46 cctgtctca tctctatgtt tgataaatct ttgtgtcgag gcgtggatgt cacacttgat 900
47 acgtatccat acttgcagg ctgtacaact ctggctgcatt tggatccaaat ttggcatct 960
48 gctggcggcc cacaagagac gcttaaaagg ttgtggatg cagaatcgag agaaaagatt 1020
49 cgtatagccg tggaaatcaa agggtgtgtat ggccgcattt gtattccaa acactggac 1080
50 gaaatccaga tcgggacgac taatgaacca tcaatgcattt cgtattctgg tcgcaggcta 1140
51 tcagaagtgg cacagtctgt tggaaagccg accatcgaaat tcttttcga gattctgaa 1200
52 aaggataagc tcgcaacgag ctgtatcatg catgttggca atgaagaaaa cgtccgacag 1260
53 atcatgcacg atcgggtcca tatggcaggc agtgtatggta tcttgcacgg gcagacgcta 1320
54 caccgcacgatttgcac attcacgcgg tatttaggac actattctcg tgaactctcg 1380
55 ctgttgcctc tgccgtccat gatgcgtcac cttacatcac ggccgcctaa acgactttcg 1440
56 gtatatccat atcgccgtct gattgtgtat ggatccgcgtt cgcacattgtt ggttttaac 1500
57 cccgaaacgg taaagatgtt gtcgacgtat gaagacccaa aggtgcctaa tcggggcatt 1560
58 agatttggc tagttaacgg ccagatagct gtggacgaaag gcaagatgac aggacacaaga 1620
59 gggggtaaaa cactgagaag aagcaccat ggcaaggatga aggcaagaga tggat 1677

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001
TIME: 13:48:46

Input Set : A:\06501-072001.txt
Output Set: N:\CRF3\07252001\I770517.raw

61 <210> SEQ ID NO: 2
 62 <211> LENGTH: 558
 63 <212> TYPE: PRT
 64 <213> ORGANISM: Hypomyces mycophilus
 66 <400> SEQUENCE: 2
 67 Met Arg Thr Glu Ile Leu Phe His Ser Ala Thr Val Ile Thr Gly Asp
 68 1 5 10 15
 69 Glu Ala Ala Gln Pro Phe Val Ala Asp Val Leu Val Ser Lys Gly Leu
 70 20 25 30
 71 Ile Ala Lys Ile Gly Asn Pro Gly Ser Ile Asn Ala Thr Pro Asp Thr
 72 35 40 45
 73 Arg His Leu Asp Val Thr Gly Tyr Ile Leu Ser Pro Gly Phe Ile Asp
 74 50 55 60
 75 Met His Ala His Ser Asp Leu Tyr Leu Leu Ser His Pro Asp His Glu
 76 65 70 75 80
 77 Ala Lys Ile Thr Gln Gly Cys Thr Thr Glu Val Val Gly Gln Asp Gly
 78 85 90 95
 79 Ile Ser Tyr Ala Pro Ile Arg Asn Val Asp Gln Leu Arg Ala Ile Arg
 80 100 105 110
 81 Glu Gln Ile Ala Gly Trp Asn Gly Asn Pro Thr Asp Glu Glu Cys Arg
 82 115 120 125
 83 Thr Thr Leu Lys Gly Val Gly Met Phe Glu Trp Gln Thr Ile Gly Glu
 84 130 135 140
 85 Tyr Leu Asp Cys Leu Glu Arg Asn Arg Thr Ala Thr Asn Val Ala Met
 86 145 150 155 160
 87 Leu Val Pro Gln Gly Asn Leu Arg Leu Leu Ala Cys Gly Pro Tyr Asp
 88 165 170 175
 89 Thr Pro Ala Ser Ala Glu Glu Ile Gln Asp Gln Ile Gln Leu Leu Arg
 90 180 185 190
 91 Glu Ala Met Ala Gln Gly Ala Val Gly Met Ser Ser Gly Leu Thr Tyr
 92 195 200 205
 93 Thr Pro Gly Met Tyr Ala Ser Thr Ser Glu Leu Ala Ser Leu Cys Ala
 94 210 215 220
 95 Ala Leu Ala Gln Glu Pro Gly Ala Phe Tyr Ala Pro His His Arg
 96 225 230 235 240
 97 Ser Tyr Gly Phe Gln Ala Ile Glu Ser Tyr Ala Glu Met Leu Asp Leu
 98 245 250 255
 99 Gly Glu Ser Thr Gly Cys Pro Ile His Leu Thr His Ala Thr Leu Asn
 100 260 265 270
 101 Phe Ser Glu Asn Lys Gly Lys Ala Pro Val Leu Ile Ser Met Val Asp
 102 275 280 285
 103 Lys Ser Leu Ala Ala Gly Val Asp Val Thr Leu Asp Thr Tyr Pro Tyr
 104 290 295 300
 105 Leu Pro Gly Cys Thr Thr Leu Ala Ala Leu Leu Pro Ser Trp Ala Ser
 106 305 310 315 320
 107 Ala Gly Gly Pro Gln Glu Thr Leu Lys Arg Leu Glu Asp Ala Glu Ser
 108 325 330 335
 109 Arg Glu Lys Ile Arg Ile Ala Val Glu Ile Lys Gly Cys Asp Gly Gly
 110 340 345 350

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001
TIME: 13:48:46

Input Set : A:\06501-072001.txt
Output Set: N:\CRF3\07252001\I770517.raw

111 His Gly Ile Pro Thr Asn Trp Asp Glu Ile Gln Ile Gly Thr Thr Asn
112 355 360 365
113 Glu Pro Ser Ile Ala Ser Tyr Ser Gly Arg Arg Leu Ser Glu Val Ala
114 370 375 380
115 Gln Ser Val Gly Lys Pro Thr Ile Glu Val Phe Phe Glu Ile Leu Gln
116 385 390 395 400
117 Lys Asp Lys Leu Ala Thr Ser Cys Ile Met His Val Gly Asn Glu Glu
118 405 410 415
119 Asn Val Arg Gln Ile Met Gln His Arg Val His Met Ala Gly Ser Asp
120 420 425 430
121 Gly Ile Leu His Gly Gln Thr Leu His Pro Arg Ala Tyr Gly Thr Phe
122 435 440 445
123 Thr Arg Tyr Leu Gly His Tyr Ser Arg Glu Leu Ser Leu Val Ala Leu
124 450 455 460
125 Pro Ser Met Ile Ala His Leu Thr Ser Arg Pro Ala Lys Arg Leu Ser
126 465 470 475 480
127 Val Tyr Pro Tyr Arg Gly Leu Ile Ala Glu Gly Ser Ala Ala Asp Ile
128 485 490 495
129 Val Val Phe Asn Pro Glu Thr Val Lys Asp Met Ser Thr Tyr Glu Glu
130 500 505 510
131 Pro Lys Val Pro Ser Arg Gly Ile Arg Phe Val Leu Val Asn Gly Gln
132 515 520 525
133 Ile Ala Val Asp Glu Gly Lys Met Thr Gly Thr Arg Gly Gly Lys Thr
134 530 535 540
135 Leu Arg Arg Ser Thr Asp Gly Lys Val Lys Ala Arg Asp Glu
136 545 550 555
138 <210> SEQ ID NO: 3
139 <211> LENGTH: 20
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
146 <400> SEQUENCE: 3
147 cccggcttca tcgacatgca 20
149 <210> SEQ ID NO: 4
150 <211> LENGTH: 20
151 <212> TYPE: DNA *OK*
152 <213> ORGANISM: Artificial Sequence
W--> 154 <220> FEATURE: misc. feature Field 220 must be blank
W--> 155 <221> NAME/KEY: (18) Field 221 must include a term from name key table 5 or 6
W--> 156 n is A,T,C, or G Field 222 must specify a location for n in the
158 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
160 <400> SEQUENCE: 4
nucleic acid sequence
W--> 161 ttcatcgaca tgcaygcaca Field 223 must include a description of n including
163 <210> SEQ ID NO: 5 possible values and any additional descriptive information
164 <211> LENGTH: 20 not to exceed 4 lines of text
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
W--> 168 <220> FEATURE: misc. feature

The types of errors shown exist throughout the Sequence Listing. Please check
subsequent sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001
TIME: 13:48:46

Input Set : A:\06501-072001.txt
Output Set: N:\CRF3\07252001\I770517.raw

W--> 169 <221> NAME/KEY: (3, 6, 15)
W--> 170 n is A,T,C, or G
172 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
174 <400> SEQUENCE: 5
W--> 175 tgngggngcrt craangcytg 20
177 <210> SEQ ID NO: 6
178 <211> LENGTH: 20
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
W--> 182 <220> FEATURE: misc. feature
W--> 183 <221> NAME/KEY: (3, 9)
W--> 184 n is A,T,C, or G
186 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
188 <400> SEQUENCE: 6
W--> 189 aangcytgng grtaytcrtc 20
191 <210> SEQ ID NO: 7
192 <211> LENGTH: 321
193 <212> TYPE: DNA
194 <213> ORGANISM: Hypomyces mycophilus
196 <400> SEQUENCE: 7
197 ttcatcgaca tgcatgcgca gctggatggt caacccgtac aactacaaca agataactctc 60
198 ttagacaaa aaatcggggg tcgtggcat gcagagcggc attcgactat acacccttg 120
199 cgaagagctg gagctacatg gcctggcaat gccaaacctg ggcagtataa acgagcaatc 180
200 catcgccggc gccatatcta caggcacaca cggcagcagc atccaccacg gcctcatgtc 240
201 tgaggatatt ctgcgtctga aatcactct cgcggcggc aagacggagg catgtccaa 300
202 agacgaatac ccccaaggct t 321
204 <210> SEQ ID NO: 8
205 <211> LENGTH: 20
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
212 <400> SEQUENCE: 8 20
213 aggccaaat caccgaagga
215 <210> SEQ ID NO: 9
216 <211> LENGTH: 20
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
223 <400> SEQUENCE: 9
224 attggggaat acttggattg 20
226 <210> SEQ ID NO: 10
227 <211> LENGTH: 20
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
234 <400> SEQUENCE: 10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001
TIME: 13:48:46

Input Set : A:\06501-072001.txt
Output Set: N:\CRF3\07252001\I770517.raw

235 ctggttcttt ccgcctcaga 20
 237 <210> SEQ ID NO: 11
 238 <211> LENGTH: 20
 239 <212> TYPE: DNA
 240 <213> ORGANISM: Artificial Sequence
 242 <220> FEATURE:
 243 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
 245 <400> SEQUENCE: 11
 246 attaaccctc actaaaggc 20
 248 <210> SEQ ID NO: 12
 249 <211> LENGTH: 1325
 250 <212> TYPE: DNA
 251 <213> ORGANISM: Hypomyces mycophilus
 253 <400> SEQUENCE: 12
 254 caggacggcc actaatgtcg ccatgttgg tccgcaaggc aacctgagat tattggcatg 60
 255 tggcccatac gatactccag catctgcaga agagattcaa gatcaaatcc agctttgcg 120
 256 agaggctatg gtcaggggt ctgtcgggat gtctagtggt ctcacttata caccggcat 180
 257 gtatgcttcc acgtcggAAC tagttctct gtgcgcggcc ctgcacaag aatttccagg 240
 258 tgcattctat ggcacatc atagaagta tgggttccag gccatcgaaa gttatgccga 300
 259 aatgttggat ctcggagagt caacaggctg tcccattcat cttacacatg caacgctcaa 360
 260 cttttcagaa aataaggta aagctcctgt cctcatctt atgggtgata aatctttgc 420
 261 tgcaggcgtg gatgtcacac ttgatacgtt tccatacttgc ccaggctgtt caactctggc 480
 262 tgcattgctg ccaagtccgg catctgctgg cggcccacaa gagacgcttta aaaggcttga 540
 263 ggatgcagaa tcgagagaaa agattctgtat agccgtggaa atcaaagggt gtgatggcgg 600
 264 ccatggattt ccaaccaact gggacgaaat ccagatccgg acgactaatg aaccatcaat 660
 265 cgcacatgtat tctggtcgcg gctatcaga agtggcacag tctgttggaa agccgaccat 720
 266 cgaagtcttt ttccggattc tgcggaaatgaa taagctcgca acgagctgtt tcattgcattgt 780
 267 tggcaatgaa gaaaacgtcc gacagatcat gcagatccgg gtccatatgg caggcgttga 840
 268 tggatcttg cacggccaga cgctacaccc acgagcttgc ggcacattca cgcggatttt 900
 269 aggacactat tctcggttgc tctcggttgc tccatgtatgc ctcacaccc 960
 270 atcacggccc gccaaacgac ttccggatata tccatatcgcc ggtctgattt ctgaaggatc 1020
 271 cgctggccgac attgtggttt ttaaccccgaa aacgtaaaag gatatgtcgatcgatgaa 1080
 272 gccaaagggtt gcaagtccgg gcatggattt tggtttagattt aacggccaga tagctgtgg 1140
 273 cgaaggcaag atgacaggca caagaggggg taaaacactg agaagaagca ccgatggcaa 1200
 274 ggtgaaggca agagatgagt aaagtctcgatcg tctgcattccg cgtgcggccac aacaggatca 1260
 275 agtgcgtcaca gcatgatacg gcaggcttgc gatgtatgc catgtcatgg gggaaatgg 1320
 276 caata 1325
 278 <210> SEQ ID NO: 13
 279 <211> LENGTH: 21
 280 <212> TYPE: DNA
 281 <213> ORGANISM: Artificial Sequence
 283 <220> FEATURE:
 284 <223> OTHER INFORMATION: Artificially Synthesized Primer Sequence
 286 <400> SEQUENCE: 13
 287 cggagagtcg acaggctgtc c 21
 289 <210> SEQ ID NO: 14
 290 <211> LENGTH: 20
 291 <212> TYPE: DNA
 292 <213> ORGANISM: Artificial Sequence

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001
TIME: 13:48:47

Input Set : A:\06501-072001.txt
Output Set: N:\CRF3\07252001\I770517.raw

L:154 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:155 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:156 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:4
L:161 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:168 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:169 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:170 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:5
L:175 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:182 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:183 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:184 M:257 W: Feature value mis-spelled or invalid, Describe feature in <223> for SEQ ID#:6
L:189 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6

STATISTICS SUMMARY
PATENT APPLICATION: US/09/770,517

DATE: 07/25/2001
TIME: 13:48:47

Input Set : A:\06501-072001.txt
Output Set: N:\CRF3\07252001\I770517.raw

Application Serial Number: US/09/770,517

Alpha or Numeric: Numeric

Application Class:

Application File Date: 01-26-2001

Art Unit: OIPE

Software Application: PatentIn

Total Number of Sequences: 27

Total Nucleotides: 5900

Total Amino Acids: 603

Number of Errors: 0

Number of Warnings: 15

Number of Corrections: 0

MESSAGE SUMMARY

256 W: 3 (Invalid Numeric Header Field)
257 W: 6 (Feature value mis-spelled or invalid)
258 W: 3 (Mandatory Feature missing)
341 W: 3 ((46) "n" or "Xaa" used)